Where do AFNI Datasets Come From?

- Method 1: Create datasets with program **to3d** [principal subject of this talk]
  - ⋆ Input files are arrays of numbers --- i.e., image files
- Method 2: Realtime input from an external image source program (e.g., directly from scanner's reconstructed images)
  - ⋆ AFNI programs like **Imon**(for I-files) and **Dimon** (for DICOM files) read image files from GE realtime EPI output, checks them for various errors, sends them into AFNI for display and formatting --- while acquisition continues
  - ⋆ Sample program **rtfeedme** can be used to write your own image source program
- Method 3: AFNI programs can read other formats for display and analysis
  - ⋆ ANALYZE™ 7.5 format ⇒ **.hdr/.img** file pairs
    - ➥ Used by SPM and many other programs
    - ➥ Major drawback: lack of spatial orientation and position information in header
      - ➩ Can be difficult to overlay ANALYZE datasets with other datasets
  - ⋆ MINC format ⇒ **.mnc** files
    - ➥ Used by software from Montreal Neurological Institute --- mnitools
  - ⋆ CTF format ⇒ **.svl** files
    - ➥ Generated from CTF MEG data analysis software package

- ⋆ Dataset stored as columns of ASCII-formatted numbers ⇒ **`.1D`** and **`.3D`** files
  - ➥ Used to store datasets when knowing where the data points are in space isn't important for the analysis
  - ➥ Example: node-wise analysis of group data on surfaces
  - ➥ Each column corresponds to one sub-brick
  - ➥ Each row corresponds to one voxel or node
  - ➥ .1D files: just columns of numbers
  - ➥ .3D files: contain an XML header with geometrical information
- ⋆ NIfTI-1 format ⇒ **`.hdr/.img`** file pairs or **`.nii`** files
  - ➥ New format, modified from ANALYZE 7.5 compatible programs
  - ➥ Supposed to be mostly compatible with ANALYZE 7.5 compatible programs
  - ➥ Format finalized late 2003; will be supported by SPM, AFNI, FSL, Brain Voyager

• <u>Method 4</u>: Output of most AFNI programs is AFNI-formatted datasets ⇒ **`.HEAD/.BRIK`** file pairs

- ⋆ AFNI utility programs exist to re-write AFNI-formatted datasets into ANALYZE, MINC, and .3D formats
- ⋆ In the future, AFNI programs will be able to write out NIfTI-1 **`.nii`** formatted datasets directly

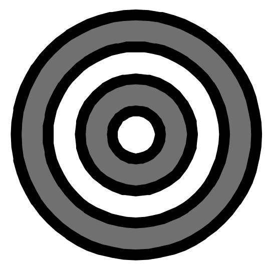
Creating AFNI Datasets with Program **to3d**

- **to3d** reads image files -- each containing 1 or more 2D slices -- and assembles them into AFNI datasets
- The collection of all the 2D slice data forms the `.BRIK` file
  - ★ An AFNI dataset can contain a single slice
- You must also provide **to3d** with some auxiliary data (for the `.HEAD` file):
  - ★ Orientation of slices in space
  - ★ Size of slices or of the voxels
  - ★ Slice offset -- where is the dataset volume located in space?
  - ★ For 3D+time datasets, you also need slice timing information
  - ★ **to3d** 'knows' how to get some of this auxiliary information from image file headers for some image file formats:
    - ➥ ANALYZE 7.5 **.hdr/.img** pairs contain voxel size information
    - ➥ Siemens **.ima** Files contain voxel size and orientation information
    - ➥ GE **I.** Files contain voxel size and orientation information
    - ➥ DICOM Files contain lots of relevant information
      - ➪ But manufacturers' variations on DICOM are frustrating

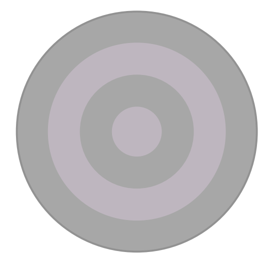
- **`to3d`** runs in two modes:
  - ★ *Command line mode:* you provide all auxiliary information on command line
  - ★ *Graphical interface (GUI) mode:* you provide auxiliary information by filling out an on-screen form
- **`Sample Study:`** data from NIH GE 3Tesla Scanner
  - ★ Files stored in directory **`AFNI_data1/`**
  - ★ Anatomical (SPGR) data ⇒ 3D dataset (no time; 1 sub-brick)
    - ➥ 124 sagittal slices in subdirectory **`SPGR_anat/`**
  - ★ Functional (EPI) time series data ⇒ 3D+time dataset (110 sub-bricks or time pts)
    - ➥ 2970 images (27 sagittal slices, 110 reps) in subdirectory **`EPI_run1/`**
    - ➥ Visual motion task: Videos of moving humans and tools (Beauchamp et al, 2002):

Moving Human

Moving Tool



High Contrast Moving Grating



Low Contrast Moving Grating

- Experiment log, taken at scanner:

NIMH-LBC--Methods FMRI Research **RUN DATA**

Exp Code: DD Date/Time: March 20, 2000 9 am Investigator: Mike B.

Scanner: 3T Coil: Wong/MAI/ GE

ANAT Scan1: Type: SPGR /FSE/MPIR TE(ms):____ TR(ms):____Flip:____ FOV(mm): 240

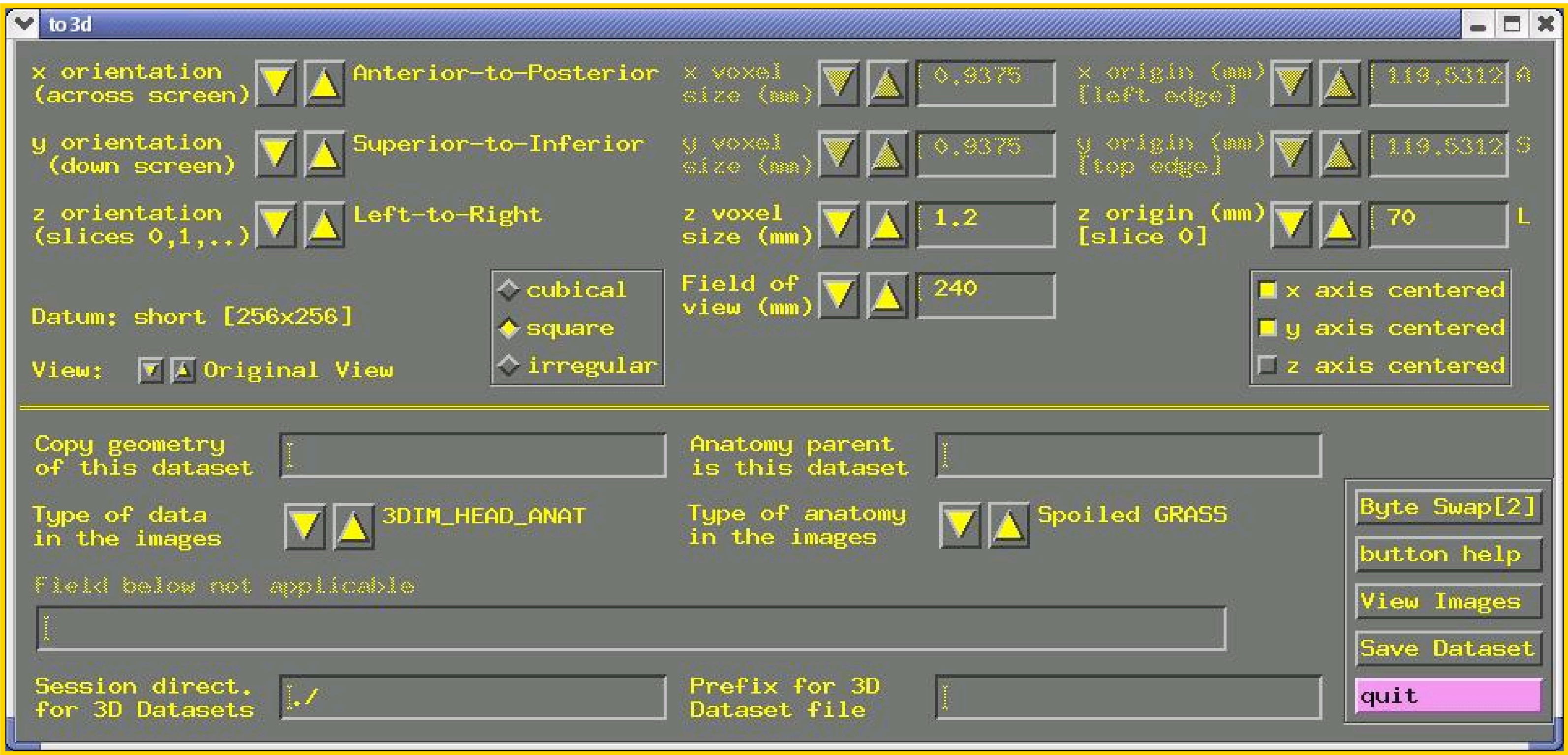
Matrix: 256x256 #slices: 124 Plane: Ax/Cor/ Sag Thickness(mm): 1.2 First: 70.0 L
Last: 77.6 R

EPI Scan: GE-EPI /SE-EPI/ GE RT EPI TE(ms):____ TR(ms): 2.5 sec Flip:___

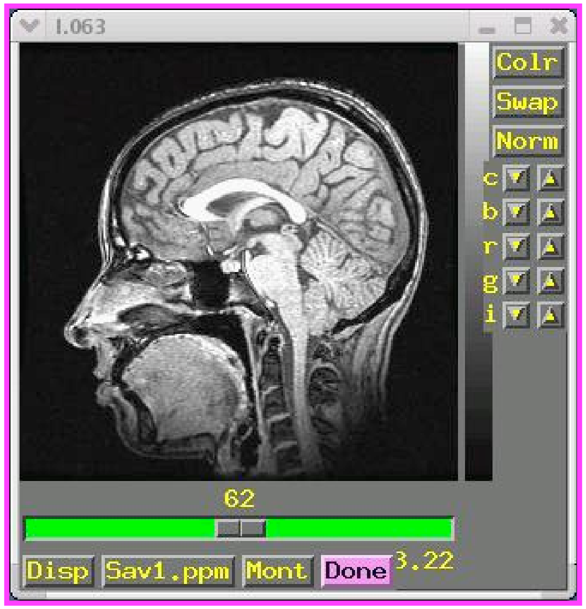
Plane: Ax/ Cor/ Sag FOV(mm): 240 Matrix: 64 Thickness(mm): 5.0
#slices: 27 (110 reps each) First: 69.0 R Last: 61.0 L

Run#	Time	Conditions	Stimulus File	Data File	Response File
1			001/I.001 ---> 041/I.972		(block design)
2			041/I.973 ---> 101/I.945		
3			101/I.946 ---> 161/I.918		
4			161/I.919 ---> 221/I.891		

- Using **to3d** to assemble the SPGR dataset:
  - ★ **cd AFNI_data1/SPGR_anat** ⇒ change directory, to get at images
  - ★ **ls** ⇒ to see what files are there (should see `I.001 . . . I.124`)
  - ★ **to3d I.*** ⇒ run **to3d**, reading in all the images files --- GUI pops us:

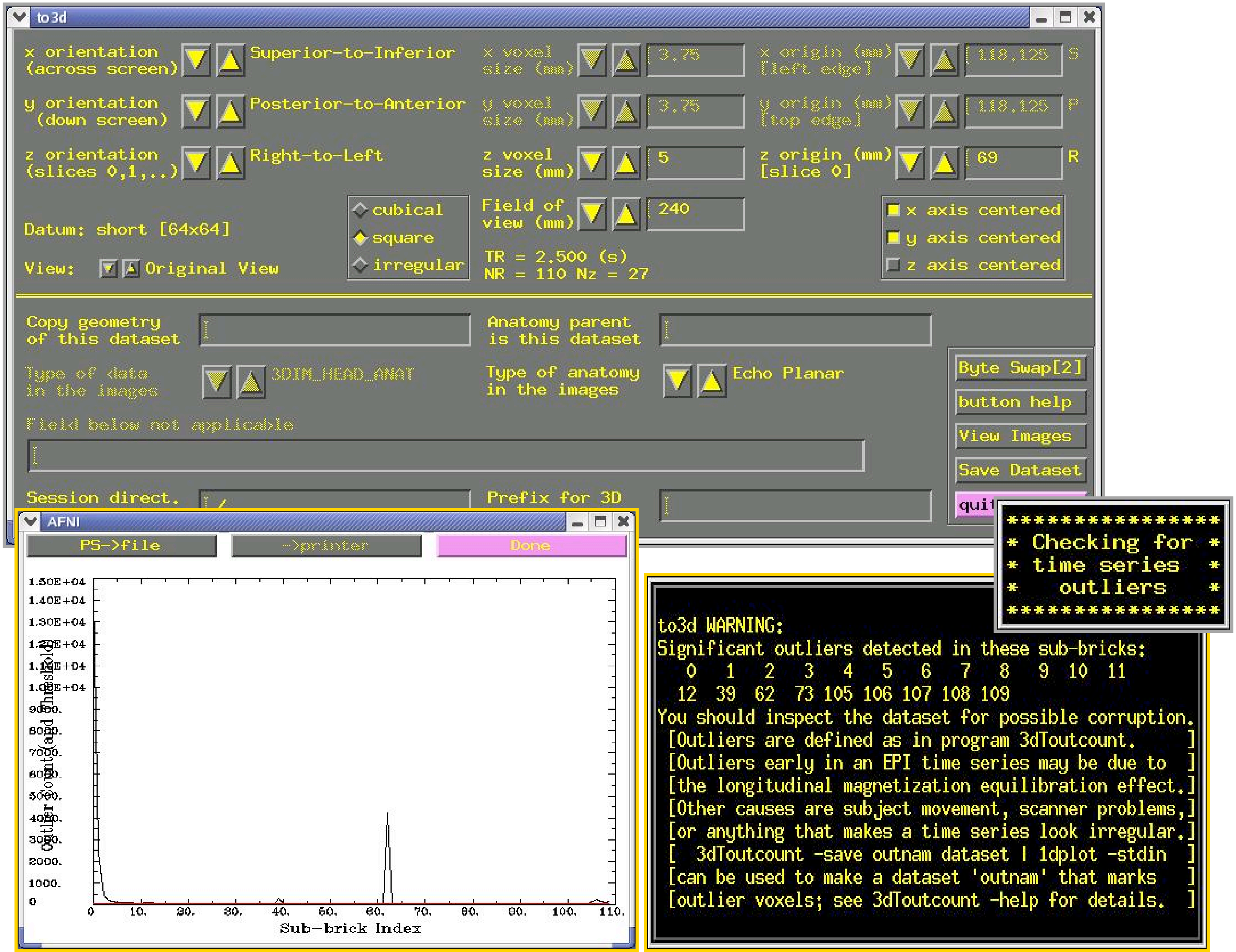


- ➥ **to3d** understands **GE I.*** files, and so has filled in some of the GUI
- ➥ Note: z-origin field **70.0 L** corresponds to experiment log



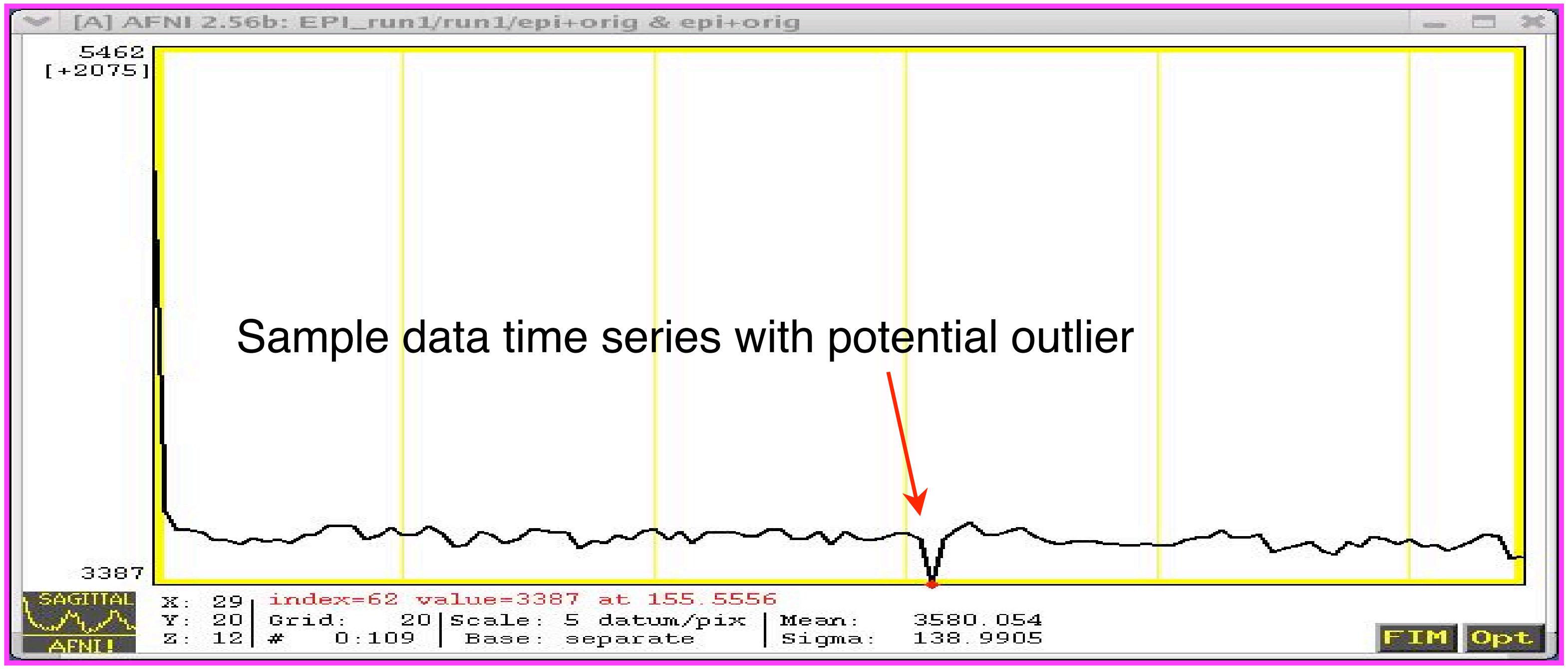
- ★ To check images that were just input, click the [View Images] button in the **to3d** GUI
  - ➥ Window is the same as the AFNI image viewer
  - ➥ Slider below image lets you move between slices
- ★ In this example, **to3d** has all the information needed from the **I.*** headers
  - ➥ All you need to do is supply the data Prefix , then press [Save Dataset]
    - ➭ Look at the bottom right of the **to3d** GUI for these controls
    - ➭ I suggest the prefix **anat**
  - ➥ Dataset files **anat+orig.HEAD** and **anat+orig.BRIK** will be created
  - ➥ Then press [quit] button *twice* to exit **to3d** GUI
- ★ Script version (no GUI): **to3d -prefix anat I.*** would create a dataset with no user intervention
- ★ Later: will give a more complicated example of assembling data from 'naked' image files, where no header information is available

- Using **to3d** to assemble the EPI 3D+time dataset:
  - ★ **`cd ../EPI_run1`** ---> change directory to get at images
  - ★ **`ls`** ---> to see what files are there (should see files `I.0001 . . . I.2970`)
  - ★ We do not just do **`to3d I.*`** to create a 3D+time dataset
  - ★ For historical reasons, the time-axis information must be given on the **`to3d`** command line.
    - ➥ Cannot be modified from the GUI
  - ★ Command line: **`to3d -time:zt 27 110 0 alt+z I.*`**
    - ➥ `-time:zt` ⇒ slices usually presented in order of space (z), then time (t)
      - ➪ `-time:tz` is needed at some sites
      - ➪ If in doubt, do **`to3d I.*`** or **`aiv I.*`**, use viewer to look at slices and see their order [aiv = AFNI Image Viewer program]
    - ➥ `27 110` ⇒ there are 27 slices in z and 110 in t (2970 total)
    - ➥ `0` ⇒ the TR for volume acquisition will be read from the image headers
      - ➪ If not available, could put `2.5s` or `2500` instead of this `0`
    - ➥ `alt+z` ⇒ slices are gathered in alternating order in the +z direction
      - ➪ Most EPI acquisitions are really 2D multislice, spread out through time
      - ➪ AFNI header can contain information about slice timing offsets
      - ➪ Other possible modes: `zero` (for 3D), `@filename` (to specify each slice)

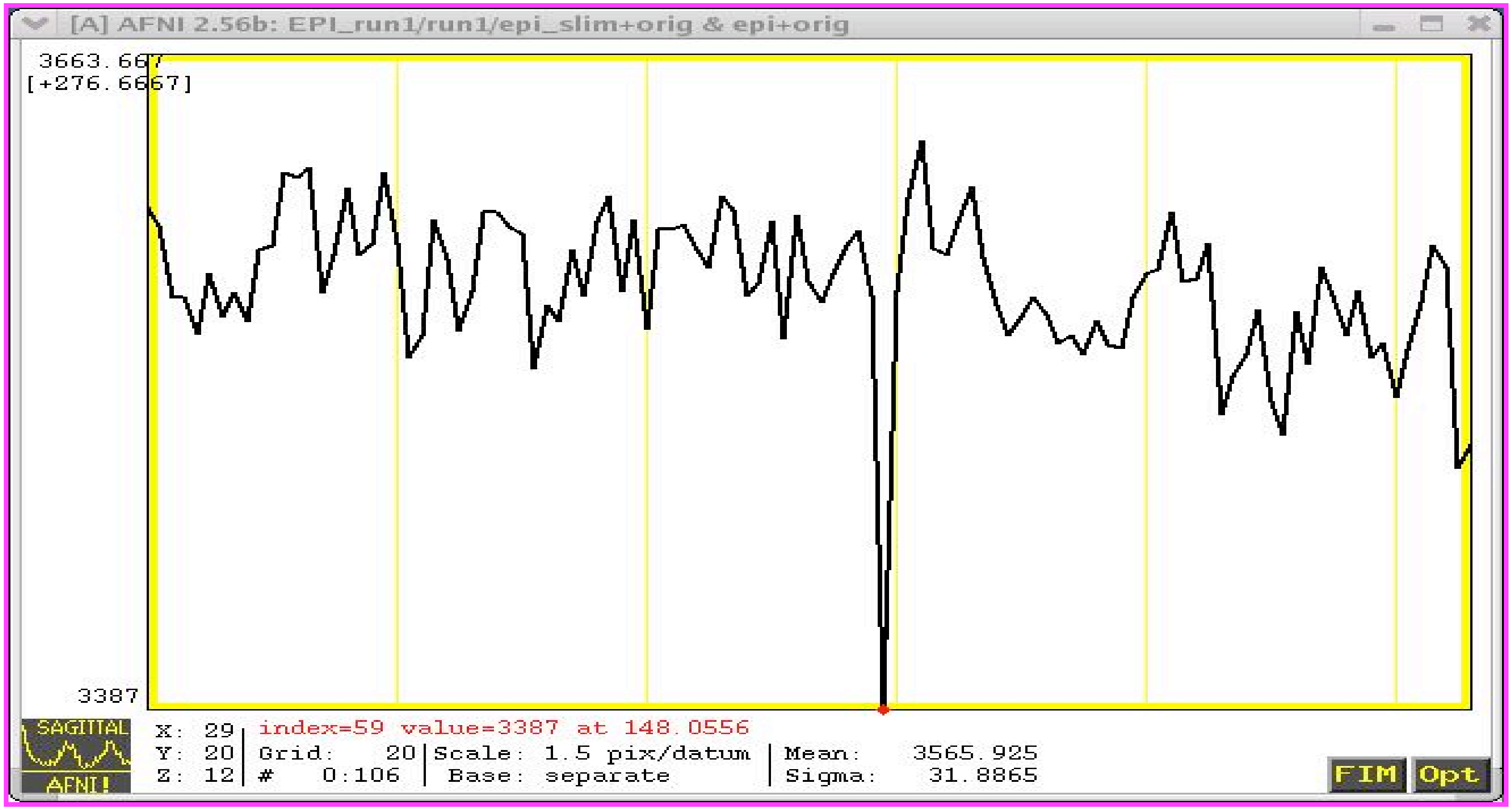

to3d
x orientation (across screen)
Superior-to-Inferior
x voxel size (mm)
3.75
x origin (mm) [left edge]
118.125
S
y orientation (down screen)
Posterior-to-Anterior
y voxel size (mm)
3.75
y origin (mm) [top edge]
118.125
P
z orientation (slices 0,1,..)
Right-to-Left
z voxel size (mm)
5
z origin (mm) [slice 0]
69
R
cubical
square
irregular
Field of view (mm)
240
x axis centered
y axis centered
z axis centered
Datum: short [64x64]
View: Original View
TR = 2.500 (s)
NR = 110 Nz = 27
Copy geometry of this dataset
Anatomy parent is this dataset
Type of data in the images
3DIM_HEAD_ANAT
Type of anatomy in the images
Echo Planar
Field below not applicable
Byte Swap[2]
button help
View Images
Save Dataset
Session direct.
Prefix for 3D
AFNI
PS->file
->printer
Done
Sub-brick Index
****
* Checking for *
* time series *
* outliers *
****
to3d WARNING:
Significant outliers detected in these sub-bricks:
0 1 2 3 4 5 6 7 8 9 10 11
12 39 62 73 105 106 107 108 109
You should inspect the dataset for possible corruption.
[Outliers are defined as in program 3dToutcount.]
[Outliers early in an EPI time series may be due to]
[the longitudinal magnetization equilibration effect.]
[Other causes are subject movement, scanner problems,]
[or anything that makes a time series look irregular.]
[3dToutcount -save outnam dataset | 1dplot -stdin]
[can be used to make a dataset 'outnam' that marks]
[outlier voxels; see 3dToutcount -help for details.]

★ **Outliers** are data values that are very different from other values in the same time series

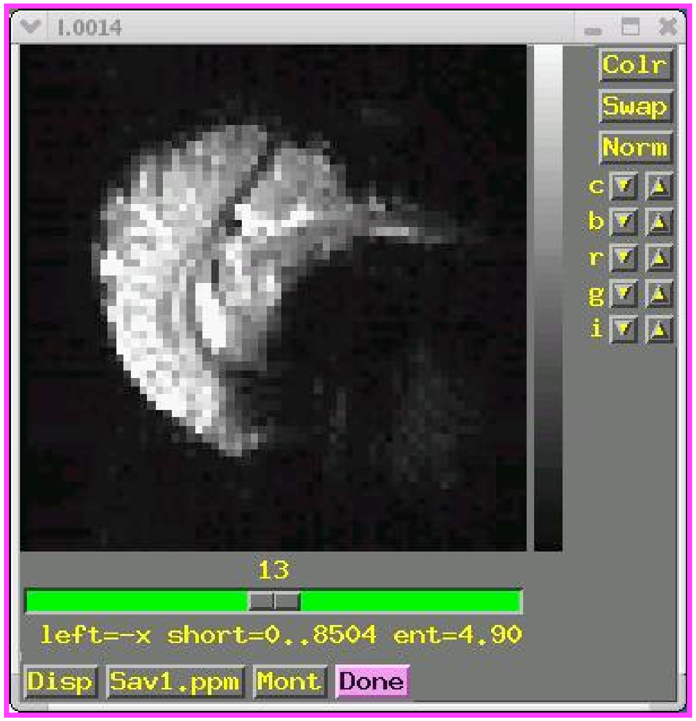
- **`to3d`** reports sub-bricks (time points) that have a lot of outliers
- You should use AFNI to look at these time points to see if there are major problems (e.g., head motion, scanner artifacts)
- **`to3d -skip_outliers`** option lets you skip the outlier detection step
- Utility program **`3dToutcount`** can also report outliers and can even make a dataset with the 'outlier-ness' of each voxel value



- The outlier becomes much more obvious when the first three time points of the time series (which show possible scanner artifacts) are removed:



- Again, fields in the GUI were filled from the **I.*** headers



- In this example, the EPI and SPGR datasets are both sagittal slices. However, AFNI can work with SPGR/EPI datasets that have different planes (e.g., if SPGR is coronal and EPI is axial)
  - Programs **3dresample** and **3daxialize** can rewrite datasets in new orientations
- Note slice thickness and slice offset ("z origin")
  - Values match experiment log (that's good)
- Time information is displayed in GUI, but not editable
- Have set "Type of Anatomy" to "Echo Planar"
  - Just acts as a reminder to user

- Script version: **to3d -time:zt 27 110 0 alt+z -prefix epi_r1 I.***
- Program **3drefit** can be used to change some header items in an AFNI dataset after it is created
  - Example: **3drefit -TR 1s epi_r1+orig** will change the TR of the dataset to 1 second

Creating New AFNI 3D+time Datasets with Program **Imon**

* **`Imon`** can be run during a scanning session on a ***GE scanner,*** to monitor the collection of time series **`I.*` files**. The user is notified of any missing or out-of-sequence slices
* **`Imon`** can also be run separate from scanning, either to verify the integrity of `I.*` files, or to create AFNI 3D+time datasets by using the **`-GERT_Reco2`** option
  * ★ **`Imon`** is run in command line mode
    * ➥ The **`-GERT_Reco2`** option is added to the command line so that `I.*` files examined by **`Imon`** can then be assembled into an AFNI 3D+time dataset
    * ➥ When not being used in real-time mode, the **`-quit`** option is added so that Imon will terminate after processing all of the `I.*` files

- Why not use **to3d** directly to create AFNI datasets?
  - ⋆ EPI images collected using GE's real time EPI sequence are saved in a peculiar fashion
    - ➥ Only 999 image files can be stored in a single directory
    - ➥ If a run consists of 110 volumes of 27 slices each, we have 2970 image files
    - ➥ With a limit of 999 `I.*` files per directory, a run made up of 2970 images would have to be saved in 3 separate directories (numbered **001/**, **021/**, and **041/**):
      - ➪ E.g., **001/**`I.028…I.999` + **021/**`I.001…I.999` + **041/**`I.001…I.999` = 2970 `I.*` files total
    - ➥ The second run would be stored in directories **061/**`I.001` ⇒ **101/**`I.973`, the third run in **101/**`I.974` ⇒ **161/**`I.946`, and the nightmare continues…
    - ➥ This setup already makes it difficult to delineate between runs. Now image what happens if the scanner hiccups, if you stop a scan in the middle and start a new one, or start collecting scans with a different number of slices!
- **Imon** attempts to identify complete scans from the images in those directories. It also monitors missing or out-of-order images, and generates the commands necessary to turn them into AFNI bricks using the script **GERT_Reco2**

- Using **Imon** to assemble the EPI 3D+time datasets
  - ★ **cd ../EPI_manyruns** ⇒ change directory to get at GE subdirectories containing images
  - ★ **ls** ⇒ to view the GE subdirectories containing 4 runs worth of `I.*` files
    - ➥ Directories are numbered in multiples of 20 (default naming system used by the GE scanner): `001/ 021/ 041/ 061/. . . 201/ 221/`
  - ★ Command line: **Imon -start_dir 001 -GERT_Reco2 -quit**
    - ➥ `-start_dir` specifies the starting directory where **Imon** will begin monitoring the images. In this example, our start directory is `001/`
    - ➥ `-GERT_Reco2` will create a script called '`GERT_Reco2`', similar to the one that program **Ifile** creates (for more info on **Ifile**, type **Ifile -help**).
      - ➯ The `GERT_Reco2` script may be run to create the AFNI datasets corresponding to the `I.*` files
    - ➥ `-quit` will terminate **Imon**, after all image files have been examined,
      - ➯ If `-quit` is not used, the program will forever wait for more images, until `<ctrl-c>` is used to terminate the program
  - ★ For a full list of **Imon** options, type **Imon -help**

- Output from **`Imon`** command:

```
File  Edit  View  Terminal  Go  Help
[morwen EPI_manyruns]$ Imon -start_dir 001 -GERT_Reco2 -quit

Imon running, use <ctrl-c> to quit...

-- scanning for first volume

-- first volume found
-- scanning for additional volumes...
-- run 1: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 2
7 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53
54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80
 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 10
5 106 107 108 109 110
-- run 2: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 2
7 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53
54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80
 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 10
5 106 107 108 109 110
-- run 3: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 2
7 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53
54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80
 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 10
5 106 107 108 109 110
-- run 4: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 2
7 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53
54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80
 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 10
5 106 107 108 109 110

final run statistics:
    volume info :
        slices  : 27
        z_first : 69.0000
        z_last  : -61.0000
        z_delta : -5.0000

    run #   1 : volumes = 110, first file = 001/I.028
    run #   2 : volumes = 110, first file = 061/I.001
    run #   3 : volumes = 110, first file = 101/I.973
    run #   4 : volumes = 110, first file = 161/I.946

[morwen EPI_manyruns]$
```

```
run# 1: volumes 110, first file = 001/I.028
run# 2: volumes 110, first file = 061/I.001
run# 3: volumes 110, first file = 101/I.973
run# 4: volumes 110, first file = 161/I.946
```

- **`Imon`** will search for missing or out-of-order images.
- Any errors will be noted on the screen
- The starting point for each run is reported at the end of **`Imon`**'s examination

- **ls EPI_manyruns** ⇒ to view the newly created **GERT_Reco2** script
  - ⋆ This script contains the commands that will automatically create bricks from the complete scans and store them in a newly created subdirectory called **afni/**
  - ⋆ To run the script, type **./GERT_Reco2**

- **cd afni** ⇒ to get at datasets
- **ls** ⇒ to view the AFNI 3D+time datasets:

Outbrick_r1+orig.HEAD	**Outbrick_r1+orig.BRIK**
Outbrick_r2+orig.HEAD	**Outbrick_r2+orig.BRIK**
Outbrick_r3+orig.HEAD	**Outbrick_r3+orig.BRIK**
Outbrick_r4+orig.HEAD	**Outbrick_r4+orig.BRIK**

Processing DICOM Image Files with **Dimon**

- **NIH - new file format (2005)**:
  - ★ Recently, the file format for images coming out of the GE scanners at the NIH has changed from **I-files** to **DICOM** (note: one of the 3Ts still outputs I-files).
  - ★ Hence, most images are no longer saved as I.0001, I.0002,…etc. Instead, they appear with a **.dcm** suffix. For example:

Anatomical Data:	Time Series (EPI) Data:
`3DMPRAGE-00001.dcm`	`HeadAx2DGRE-00001.dcm`
`3DMPRAGE-00002.dcm`	`HeadAx2DGRE-00002.dcm`
`3DMPRAGE-00003.dcm`	`HeadAx2DGRE-00003.dcm`
. . .	. . .
`3DMPRAGE-00124.dcm`	`HeadAx2DGRE-02280.dcm`

➥ The .dcm suffix appears for both anatomical and time series data.

➥ Irrespective of whether you're dealing with I.* files or *.dcm files, programs like **to3d** still work in the same way:

```
to3d -prefix fred_anat  I.*
to3d -prefix fred_anat  *.dcm
```

Processing DICOM Image Files with **Dimon**

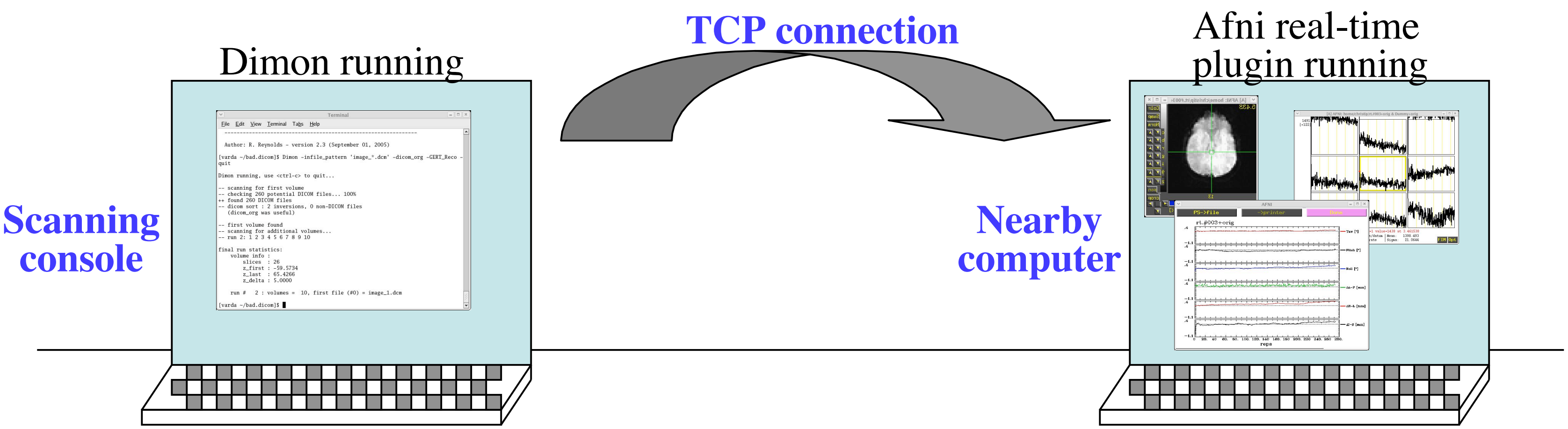
- **What is Dimon?**
  - ⋆ **Dimon** is an AFNI program (by Rick Reynolds) intended to be run in ***real time*** (i.e., during a scanning run), to monitor the collection of DICOM image files. The user will be notified of any missing slices or any slices that are acquired out of order.
    - ➥ Dimon also communicates with the realtime plugin in afni, allowing users to:
      - ➩ monitor subject head motion
      - ➩ create AFNI datasets
  - ⋆ **Dimon** can also be used ***off-line*** (i.e., away from the scanner), either to verify the integrity of `DICOM` files, or to create AFNI 3D and 3D+time datasets by using the **`-GERT_Reco`** option (or you can use `to3d`).
  - ⋆ Type **`Dimon -help`** for more information

- **Using Dimon in Real Time**

  ⋆ During a scanning session, **Dimon** looks for potential problems with the output image files. Optionally, `Dimon` can be used to send the images (collected into volumes) to afni's `realtime plugin`.

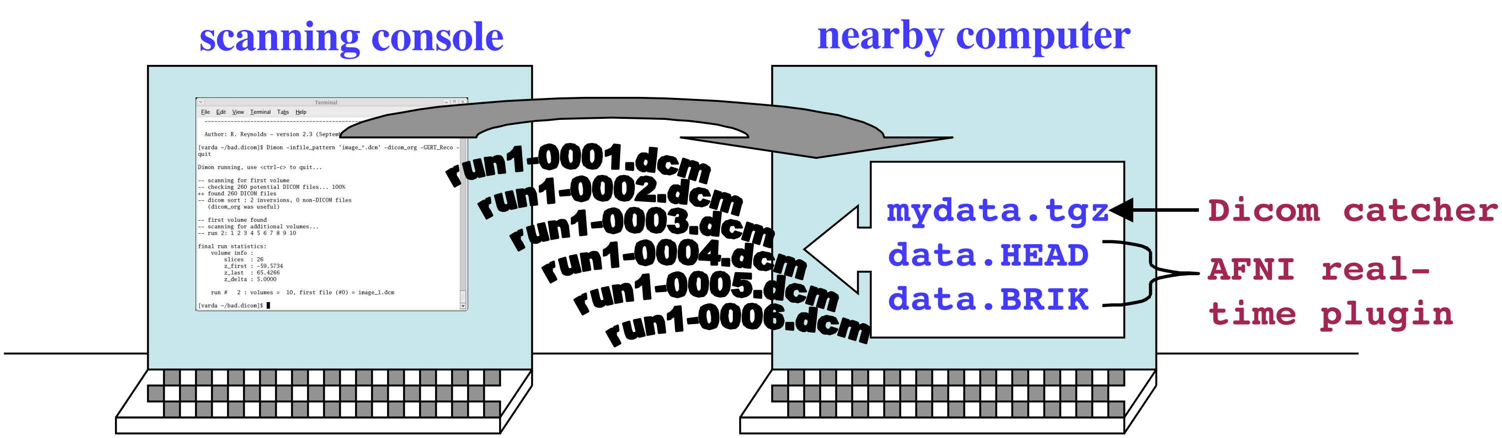
    ➥ At the NIH, `Dimon` is invoked for both of these purposes automatically.

  ⋆ If `Dimon` has established a TCP connection with the real-time plugin to `afni`, then it will send each volume to the plugin, and will notify `afni` when a single run has ended. Note that `afni` will generally be running on a *separate* computer, not the scanning console where `Dimon` runs.



  ⋆ The `realtime plugin` will show the volumes in `afni` as they arrive, along with a 3-D registration graph, allowing users to monitor subject motion.

- **<u>Overview of Real Time Processing at the NIH</u>**
  - ★ **Dimon** and `afni` are invoked automatically (via scripts written by Jerzy Borduka). No user intervention is required.
  - ★ All DICOM files are passed to the **DICOM catcher** (part of the **packrat** utilities, organized by John Ostuni). The catcher organizes the files into a directory tree, with useful filenames, and then creates a .tgz package of it.
  - ★ The incoming DICOM files are also assembled into AFNI datasets (created by afni's real-time plugin) and are available for the users to download.
    - ➥ Each EPI run (or anatomical scan) will be stored as a separate AFNI dataset (i.e., **.HEAD** and **.BRIK** files), created by the **realtime plugin**.



- **<u>Overview of Real Time Processing at the NIH</u>**
  - ★ Here is a class example of an extracted .tgz file (created by **Dicom Catcher**):

```
cd AFNI_data1/dicom/dicom.catcher/
ls 001/                      ls 002/                ls 005/
3planeloc-00001.dcm          RUN1-00001.dcm         3DFSPGRIR-00001.dcm
3planeloc-00002.dcm          RUN1-00002.dcm         3DFSPGRIR-00002.dcm
3planeloc-00003.dcm          RUN1-00003.dcm         3DFSPGRIR-00003.dcm
      . . .                      . . .                    . . .
3planeloc-00015.dcm          RUN1-00260.dcm         3DFSPGRIR-000124.dcm
```

  - ★ And here is an example of AFNI datasets (created by **AFNI Real-time Plugin**):

```
cd AFNI_data1/dicom/realtime.afni/
ls
   epiRT_scan_2#001+orig.HEAD
   epiRT_scan_2#001+orig.BRIK

    3dspgr_scan2#001+orig.BRIK
    3dspgr_scan2#001+orig.BRIK
```

  - ★ Remember, all of these files were saved on the computer that had the network connection with the computer attached to the scanning console.

- **Using Dimon OFF-LINE**
  - ★ Sometimes, it may be necessary to run **Dimon** manually from the command line.
    - ➥ Suppose you receive some DICOM files that are obviously not sorted in the proper sequential order. For example:

```
cd AFNI_data1/dicom/bad.dicom/
ls
```

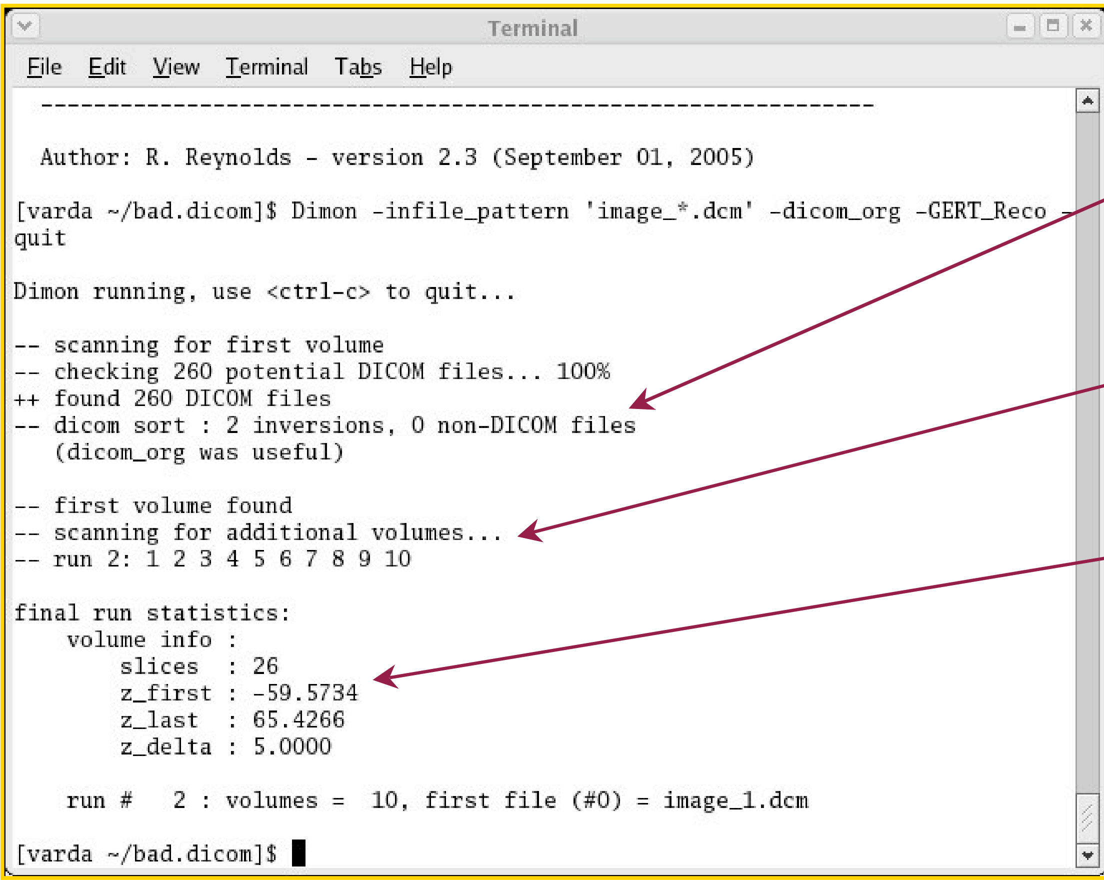
```
image_100.dcm
image_101.dcm
   . . .
image_109.dcm
image_10.dcm
image_110.dcm
image_111.dcm
   . . .
image_119.dcm
image_149.dcm
image_14.dcm, etc…
```

- The problem here is that the image number for each slice is not "zero-padded" (e.g., **image_100.dcm** instead of **image_00100.dcm**).
- When non-zero-padded files are alphabetically sorted, you get this result.
- Use the **-dicom_org** option in Dimon to re-sort them by the sequential slice and time order.
- To then assemble the images into an AFNI dataset, include the **-GERT_Reco** option on the Dimon command line.

★ Example of **Dimon** :

```
Dimon -infile_pattern 'image_*.dcm'   \
      -dicom_org -GERT_Reco -quit
```

★ <u>Output from **Dimon** command</u>:



```
Terminal
File  Edit  View  Terminal  Tabs  Help
 ---------------------------------------------------------------

 Author: R. Reynolds - version 2.3 (September 01, 2005)

[varda ~/bad.dicom]$ Dimon -infile_pattern 'image_*.dcm' -dicom_org -GERT_Reco -
quit

Dimon running, use <ctrl-c> to quit...

-- scanning for first volume
-- checking 260 potential DICOM files... 100%
++ found 260 DICOM files
-- dicom sort : 2 inversions, 0 non-DICOM files
   (dicom_org was useful)

-- first volume found
-- scanning for additional volumes...
-- run 2: 1 2 3 4 5 6 7 8 9 10

final run statistics:
    volume info :
        slices  : 26
        z_first : -59.5734
        z_last  : 65.4266
        z_delta : 5.0000

    run #   2 : volumes =  10, first file (#0) = image_1.dcm

[varda ~/bad.dicom]$
```

- DICOM files are sorted (non-DICOM files are ignored).
- Dimon looks for missing or out-of-sequence DICOM files.
- Volume information is presented when `Dimon` terminates (-quit or ctrl-c).

★ Explanation of Dimon arguments and options :

```
Dimon  -infile_pattern 'image_*.dcm'   \
       -dicom_org -GERT_Reco -quit
```

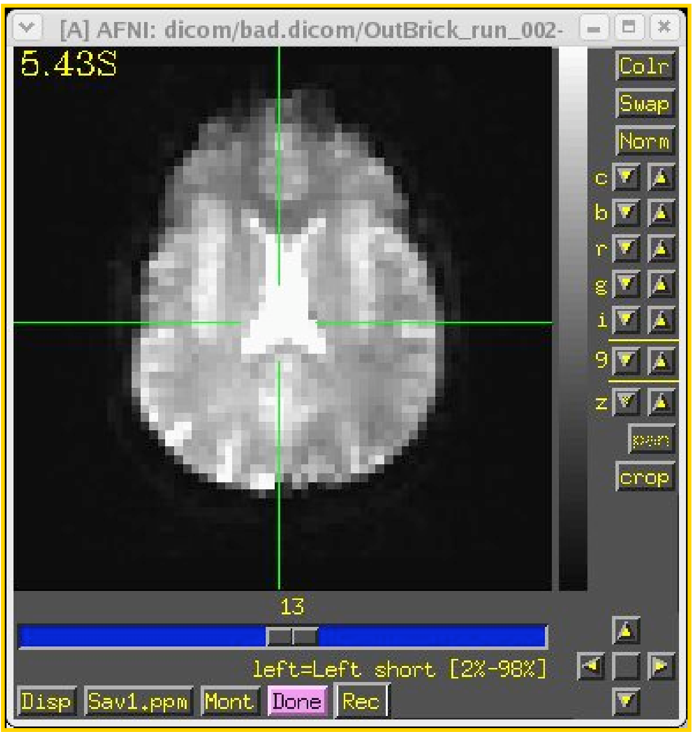
- **-infile_pattern**: This argument tells `Dimon` where the DICOM files of interest are located, and how they are labeled. In this case, the DICOM files are found in directory **AFNI_data1/dicom/bad.dicom** and they all begin with the name "**image_**" and end with the "**.dcm**" suffix.
- **-dicom_org**: This option tells `Dimon` to read the files specified by the `-infile_pattern` argument, and to determine if they are indeed DICOM files, and if so, to organize them in an ordered list of files per run.
- **-quit**: will terminate **Dimon**, after all image files have been examined,
  - If `-quit` is not used, the program will forever wait for more images, until `<ctrl-c>` is used to terminate the program
- **-GERT_Reco**: This option creates the **GERT_Reco_dicom** script in the same directory that `Dimon` was run. To create AFNI datasets, just execute this script:

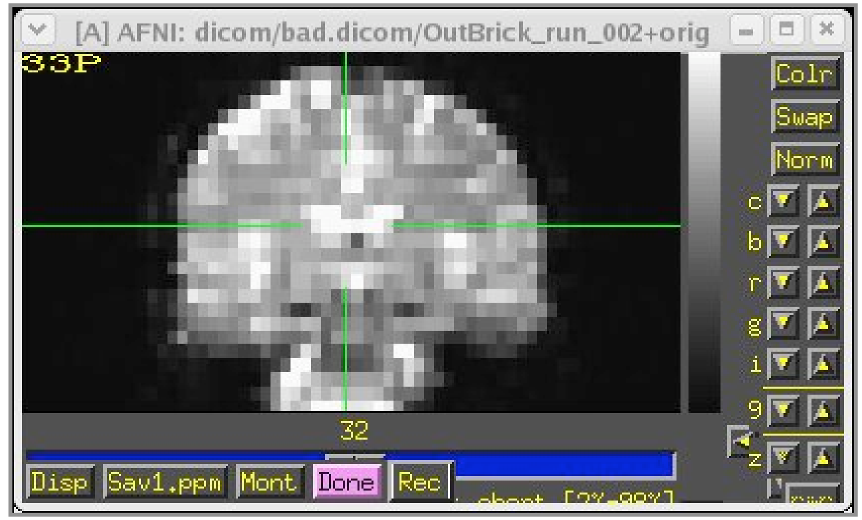
./GERT_Reco_dicom or **tcsh GERT_Reco_dicom**

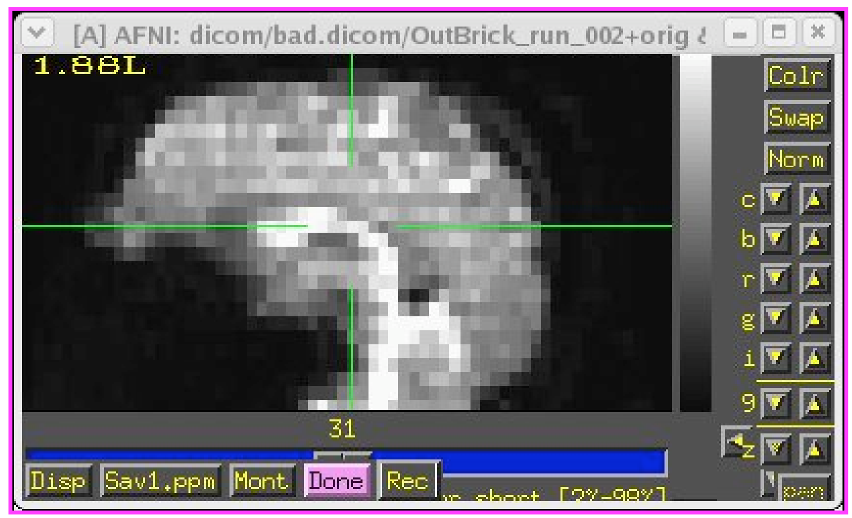
★ The result is an AFNI dataset created from the images in directory **bad.dicom/**

OutBrick_run_002+orig.HEAD

OutBrick_run_002+orig.BRIK

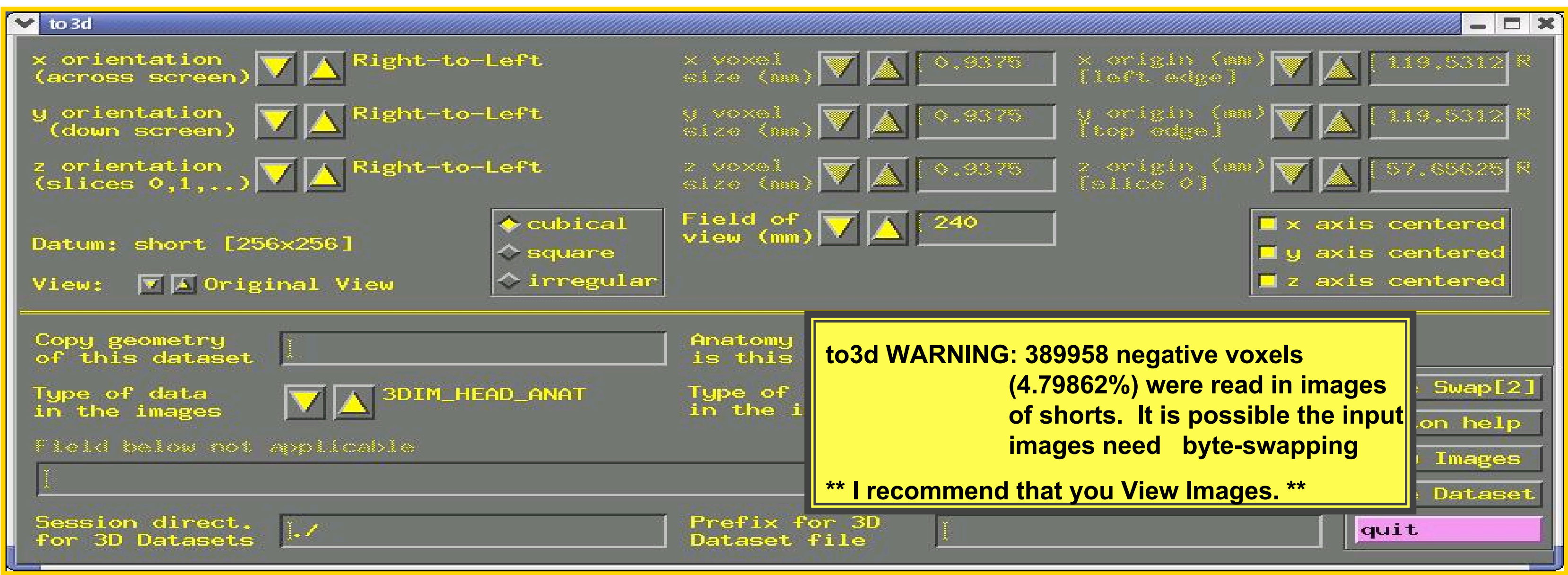


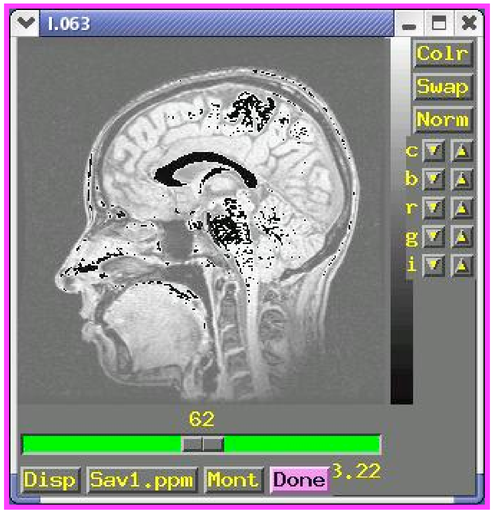




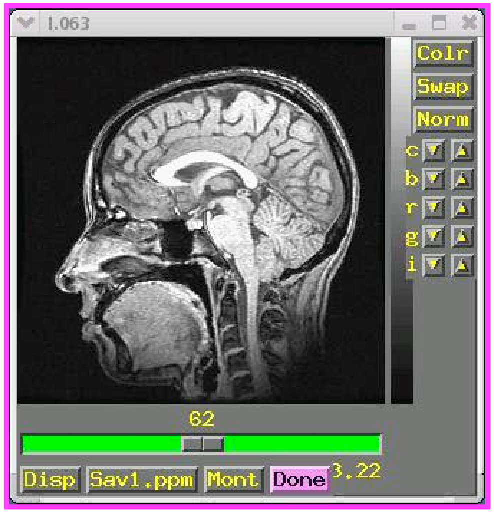
Assembling 'Naked' Images into AFNI Datasets

- 'Naked' image ⇒ image file without header data that AFNI understands
- User must supply geometrical information to **to3d**
  - ★ This is when the written experiment log is critical!
- The **SPGR_naked/** directory contains the same SPGR images as before, but stripped of all header information
  - ★ Each file has 131072 bytes = 256 x 256 16-bit integers ('shorts')
  - ★ **cd ../../SPGR_naked** (to get at images N.001...N.110), then **to3d N.***





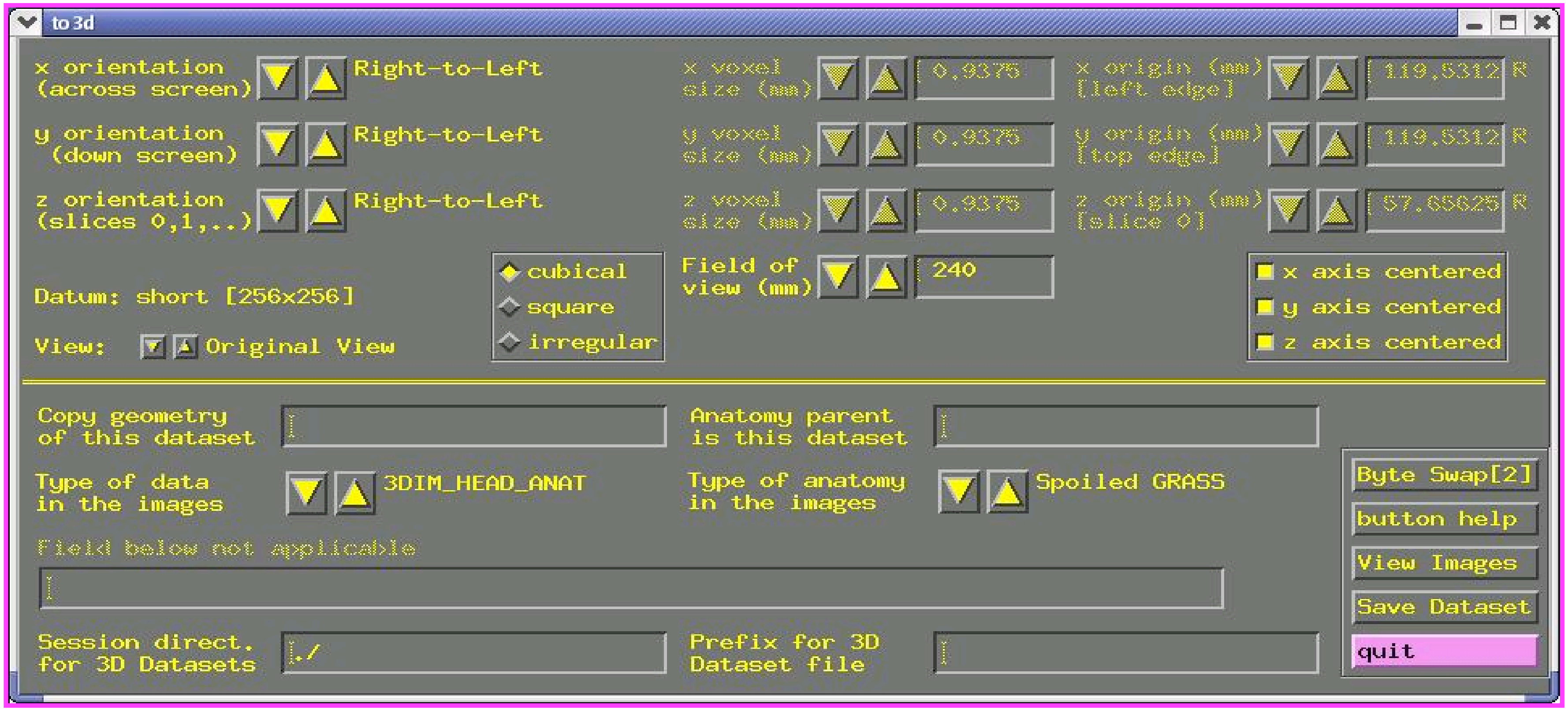
Linux/Intel computers



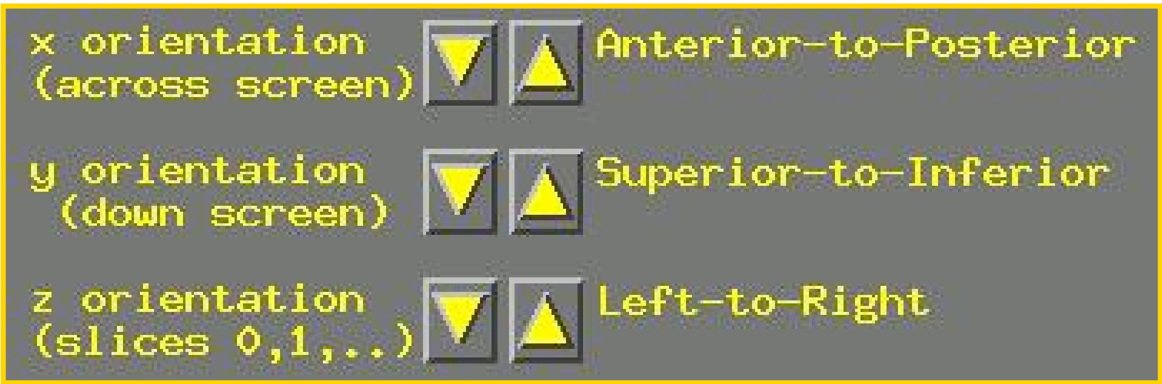
SGI/Sun/etc. computers

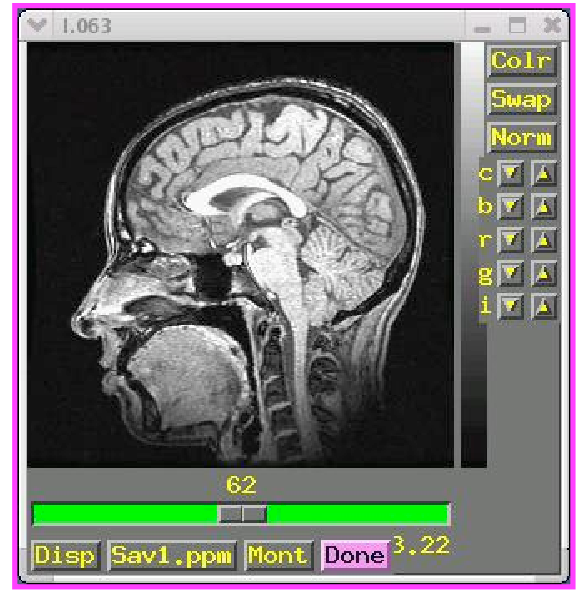
- On Linux/Intel computers: the peculiar appearance of images shows that something is wrong:
  - ⋆ MR images from scanners that are stored as shorts: 2 bytes per number
  - ⋆ Like a 2-digit decimal number: “93” means “9 x 10 + 3”
    - ➥ By universal custom, we write the “9” first
    - ➥ Could also write the same number as “39” (if we had a different custom)
  - ⋆ Customs for computers are not so universal
    - ➥ Sun and SGI systems store 2 byte numbers in reverse order from Intel
    - ➥ Result is that numbers are mangled (and some show up as negative)
    - ➥ Solution: press **`to3d`**’s **[Byte Swap[2]]** button and images are fixed!

* Same **to3d** control panel (without negative voxel warning):

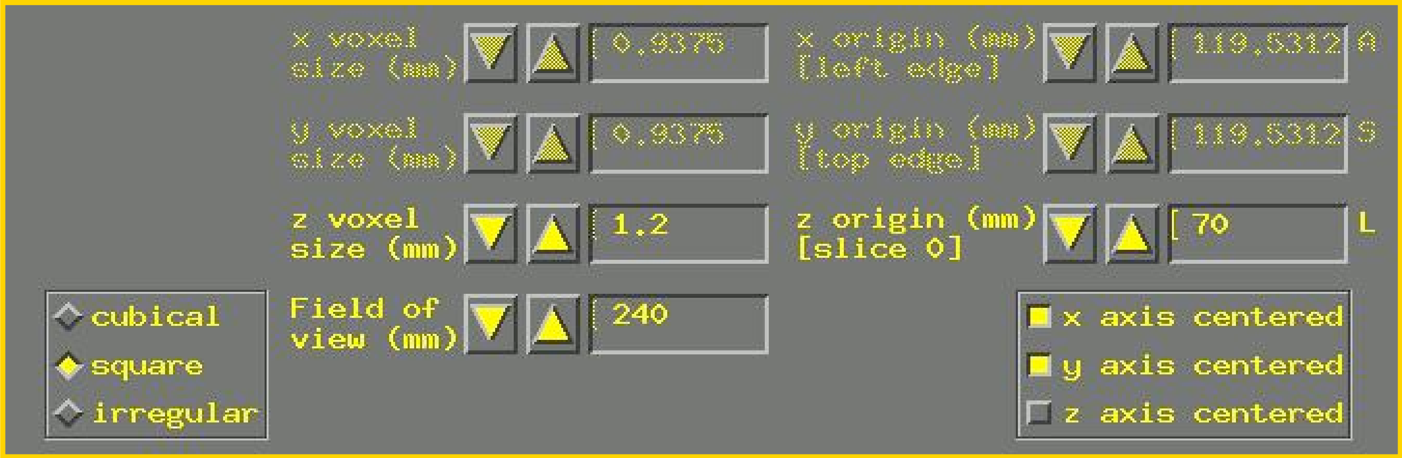


* Above the double line: must fill out 3 types of geometry information
  * ★ Left column: orientation of the dataset axes
  * ★ Middle column: size of the dataset images or voxels
  * ★ Right column: offset of the first slice





- Screen shot above shows correct orientation for this dataset
  - ⋆ Use the image viewing window to judge how images are laid out
  - ⋆ Click the arrows to scroll through the 6 possible options for each orientation to set correct values
  - ⋆ “x orientation” of dataset is across the screen (Anterior to Posterior)
  - ⋆ “y” orientation of dataset is down the screen (Superior to Inferior)
  - ⋆ “z” orientation” of dataset is in increasing slice order (from Left to Right)
    - ➥ Must know subject’s right from left (from experiment log sheet or vitamin E tablet placed on one side of the head)
    - ➥ Determine this by using the slider at the bottom of image window



- To set dataset geometrical size/location, experiment log sheet is essential
- Screen shot above shows setting slice thickness to **1.2 mm**
  - ★ Default Field of view (FOV) of **240 mm** is correct for these images
  - ★ The default voxel geometry is "cubical", which is incorrect for this example
  - ★ Must set geometry to "**square**" (x size = y size, z size different)
  - ★ Then set "z voxel size" to correct value (by typing in box)
- Screen shot shows setting of first slice to **70.0 mm in Left (L)** direction
  - ★ Default is that slices are centered in the magnet
  - ★ This default is usually not the case in the z direction
  - ★ Click "z axis centered" off
  - ★ Enter offset (here 70.0 mm) into the "z origin" box

- Final required steps:
  - ★ Enter prefix for new dataset into **[Prefix]** text box at lower right of **`to3d`** control window
    - ➥ Choosing a good prefix is important for keeping datasets organized
  - ★ Press **[Save Dataset]** button
  - ★ Press **[quit]** (twice) to exit **`to3d`**
  - ★ The new dataset files should show up when you use command **`ls`**
  - ★ For organizational purposes, you may want to move your datasets to some other directory

- Geometry parent lets you copy the geometry data from a pre-existing dataset and apply it to the dataset now under construction
  - ★ Enter name of pre-existing dataset into **[Copy geometry of this dataset]** field
    - ➥ If in another directory, you must include that in the filename
  - ★ When you press 'Enter' or move the cursor from the text-entry field, **`to3d`** tries to read geometry parent dataset header
  - ★ If geometry parent has same spatial dimensions as current dataset, all geometry fields will be filled out
    - ➥ Does not affect the time fields, which must still be set using **`-time:zt`** or **`-time:tz`** on the command line
  - ★ Geometry parent very useful when constructing multiple EPI datasets from a single scanning session
- Using **`to3d`** in command line mode
  - ★ You can specify all needed inputs to to3d by using command line options
    - ➥ For a full list of options, type **`to3d -help`**
  - ★ If enough information is present on command line to define a dataset, then the GUI will not be opened, and the dataset will be written to disk
    - ➥ If the command line is incomplete, then the GUI will be opened

★ For the SPGR dataset example ('naked' image files):

```
to3d -xFOV 120A-P -yFOV 120S-I -zSLAB 70.0L-77.6R \
           -prefix anatNaked -2swap -spgr N.*
```

- `-xFOV 120A-P` says that the x axis of the images runs from 120 mm Anterior to 120 mm Posterior
- `-yFOV 120S-I` says that the y axis of the images runs from 120 mm Superior to 120 mm Inferior
- `-zSLAB 70.0L-77.6R` says that the z axis of the slices runs from 70 mm Left to 77.6 mm Right
  - `FOV` refers to the coordinates of the outer edge of the first voxel to the outer edge of the last voxel along the relevant axis (x and y, in most cases)
  - `SLAB` refers to coordinates of the center of the outermost voxels (z=slice direction, in most cases)
- `-prefix anatNaked` gives the prefix for output dataset filenames (in this case, **`anatNaked+orig.HEAD`** and **`anatNaked+orig.BRIK`**)
- `-2swap` means to byte-swap the images while reading them
- `-spgr` means to label this data as being of SPGR (SPoiled GRass) type
- `N.*` means to read the images from the files whose names start with string "N." and end with anything ("`*`" is a wildcard)

- ★ For the EPI dataset example (if image files were 'naked'):

```
to3d -xFOV 120S-I -yFOV 120P-A -zSLAB 69.0R-61.0L -2swap \
     -time:zt 27 110 2500 alt+z -prefix epiRun1 -epan I.*
```

  (this is all on one command line)

  - ➥ Options (with their arguments) can appear in any order
  - ➥ Input image filenames always appear last (i.e., `I.*` or `*.dcm`)

- <u>Conclusion</u>
  - ★ With practice, command line usage for **to3d** becomes more useful than the GUI
    - ➥ Usually need to create many datasets at once
    - ➥ Can put commands in a script file and execute them
    - ➥ Then edit the file to change a few things, and run it again
  - ★ Just create the file with your favorite UNIX text editor (emacs, nedit, vi), typing each command on a separate line
    - ➥ Long commands can be split across multiple lines by ending all but the last line with the "\" character
    - ➥ There <u>must not</u> be a blank after the "\"!!!
  - ★ You can execute a script file by typing a command like `tcsh <filename>`, which just means to read commands from "filename"
  - ★ As time goes on, you build up a set of scripts that automate various tasks for you, and ensure you do things the same way each time